

Resource Summary Report

Generated by [RRID](#) on Aug 8, 2026

Microfluidic trapping chip for culture and assay of cell clusters and objects

RRID:SCR_026069

Type: Tool

Proper Citation

Microfluidic trapping chip for culture and assay of cell clusters and objects
(RRID:SCR_026069)

Resource Information

URL: <https://patents.google.com/patent/WO2019079714A1/en>

Proper Citation: Microfluidic trapping chip for culture and assay of cell clusters and objects (RRID:SCR_026069)

Description: Microfluidic cartridge for automatically hydrodynamically loading objects (e.g., cell clusters) into traps in parallel trapping channels with one object per trap. This improves loading of cell clusters compared to well-based systems.

Resource Type: instrument resource

Defining Citation: [PMID:33472944](#)

Keywords: Microfluidic cartridge, automatically hydrodynamically loading objects, parallel trapping channels, one object per trap,

Resource Name: Microfluidic trapping chip for culture and assay of cell clusters and objects

Resource ID: SCR_026069

Record Creation Time: 20241121T053249+0000

Record Last Update: 20260808T190736+0000

Ratings and Alerts

No rating or validation information has been found for Microfluidic trapping chip for culture and assay of cell clusters and objects.

No alerts have been found for Microfluidic trapping chip for culture and assay of cell clusters and objects.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Palamides P, et al. (2016) A mouse model for ulcerative colitis based on NOD-scid IL2R^{-/-} null mice reconstituted with peripheral blood mononuclear cells from affected individuals. *Disease models & mechanisms*, 9(9), 985.

Nurizzo D, et al. (2016) RoboDiff: combining a sample changer and goniometer for highly automated macromolecular crystallography experiments. *Acta crystallographica. Section D, Structural biology*, 72(Pt 8), 966.

Johnson GT, et al. (2015) cellPACK: a virtual mesoscope to model and visualize structural systems biology. *Nature methods*, 12(1), 85.

Daniluk P, et al. (2015) WeBIAS: a web server for publishing bioinformatics applications. *BMC research notes*, 8, 628.

Zaytsev YV, et al. (2014) CyNEST: a maintainable Cython-based interface for the NEST simulator. *Frontiers in neuroinformatics*, 8, 23.

Sobolev A, et al. (2014) Data management routines for reproducible research using the G-Node Python Client library. *Frontiers in neuroinformatics*, 8, 15.

Oberlin AT, et al. (2013) Biological database of images and genomes: tools for community annotations linking image and genomic information. *Database : the journal of biological databases and curation*, 2013, bat016.

Staiger C, et al. (2013) Current composite-feature classification methods do not outperform simple single-genes classifiers in breast cancer prognosis. *Frontiers in genetics*, 4, 289.

Carreer WJ, et al. (2013) A Computational Framework for High-Throughput Isotopic Natural Abundance Correction of Omics-Level Ultra-High Resolution FT-MS Datasets. *Metabolites*, 3(4), 853.

Guziolowski C, et al. (2013) Exhaustively characterizing feasible logic models of a signaling network using Answer Set Programming. *Bioinformatics (Oxford, England)*, 29(18), 2320.

Penkett CJ, et al. (2010) Straightforward and complete deposition of NMR data to the PDBe. *Journal of biomolecular NMR*, 48(2), 85.